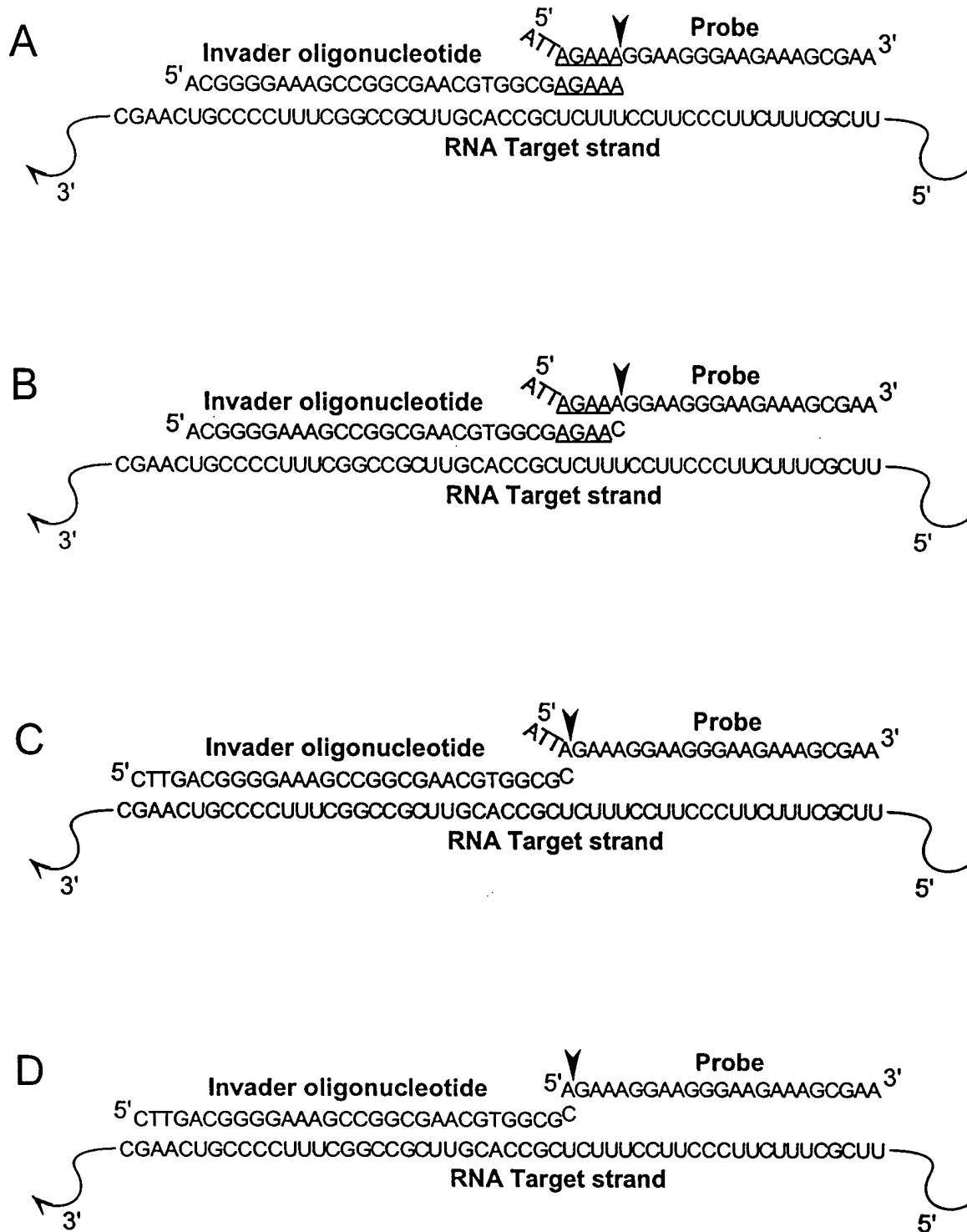


FIGURE 1

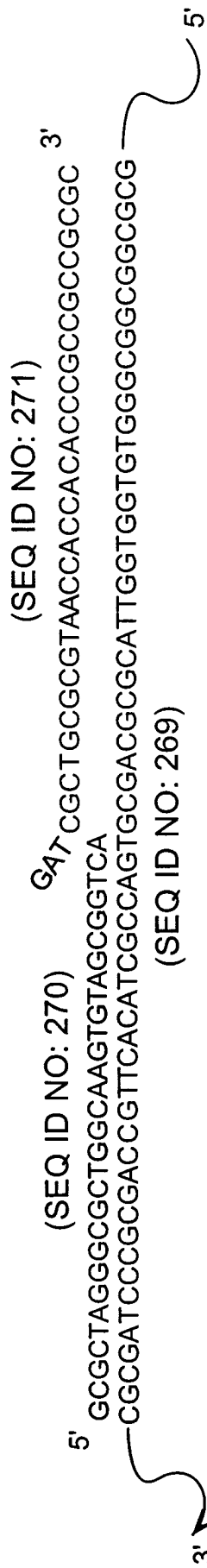
004250 402 2500

FIGURE 2



09577304-05400

A



B

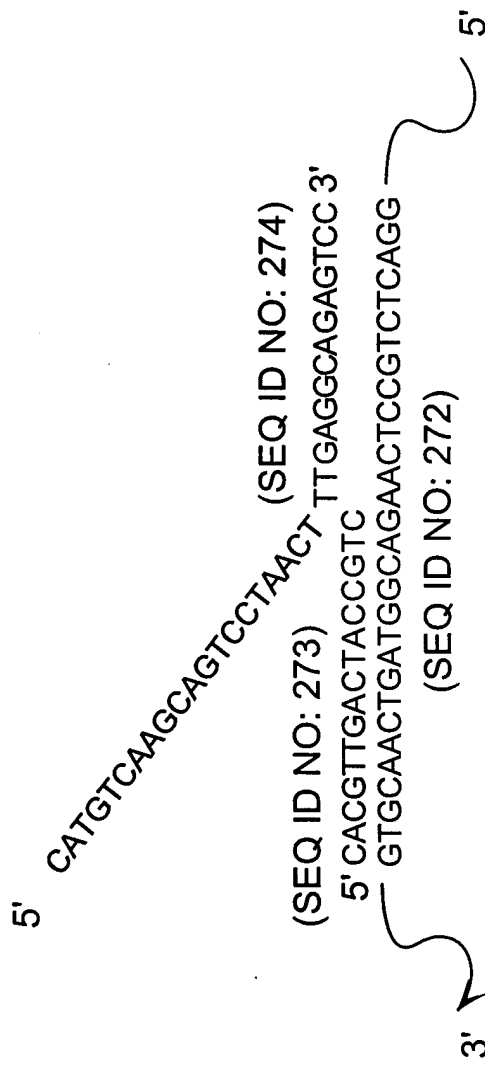


FIGURE 3

004390 #022560

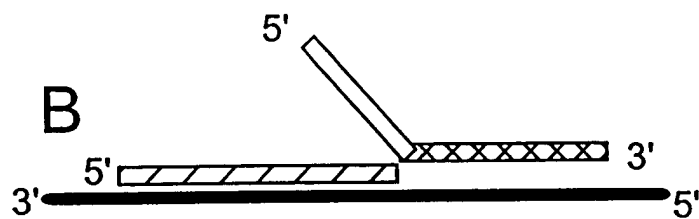
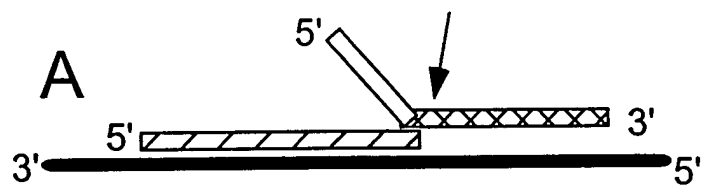


FIGURE 4

09577304 052403

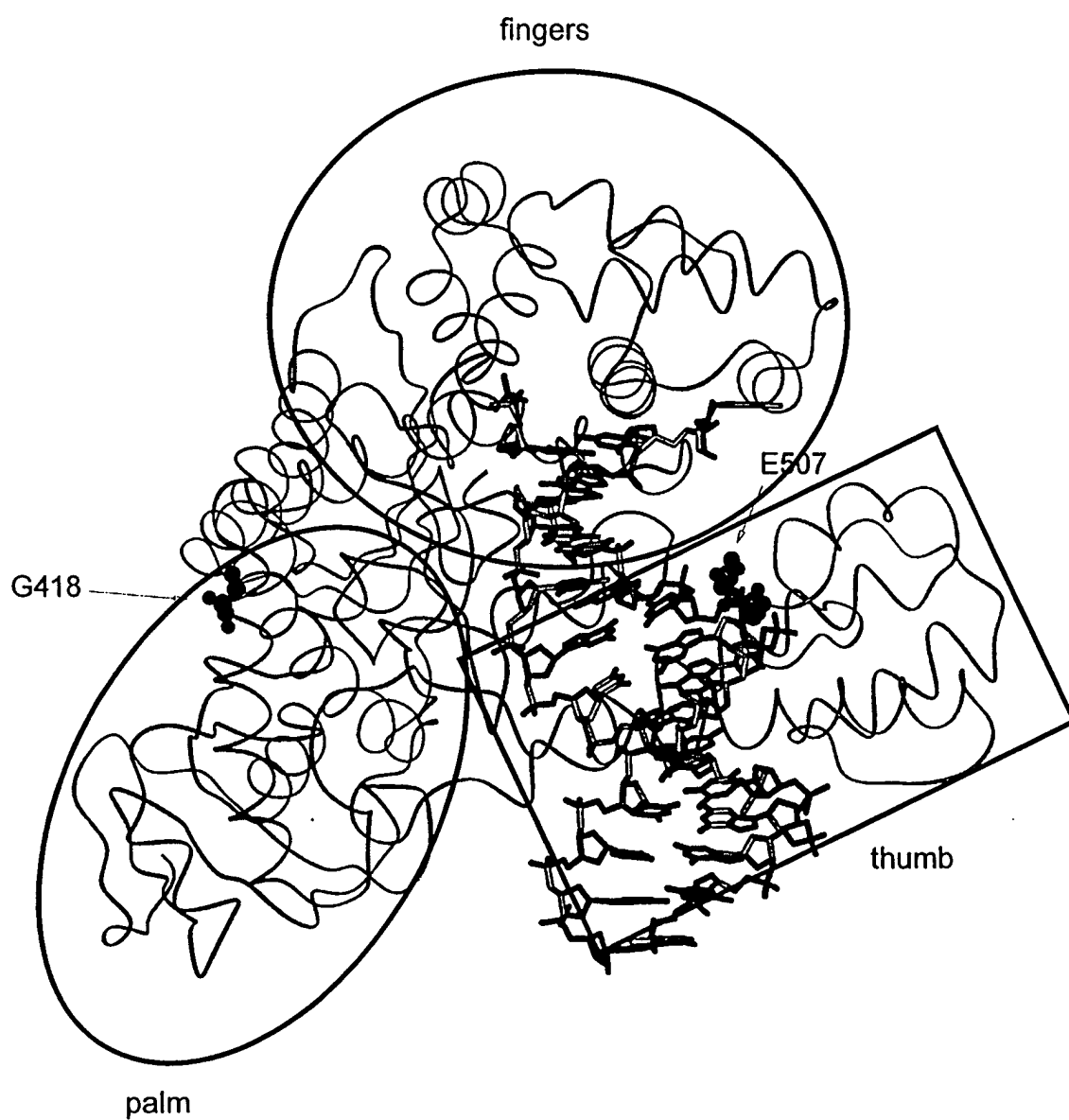


FIGURE 5

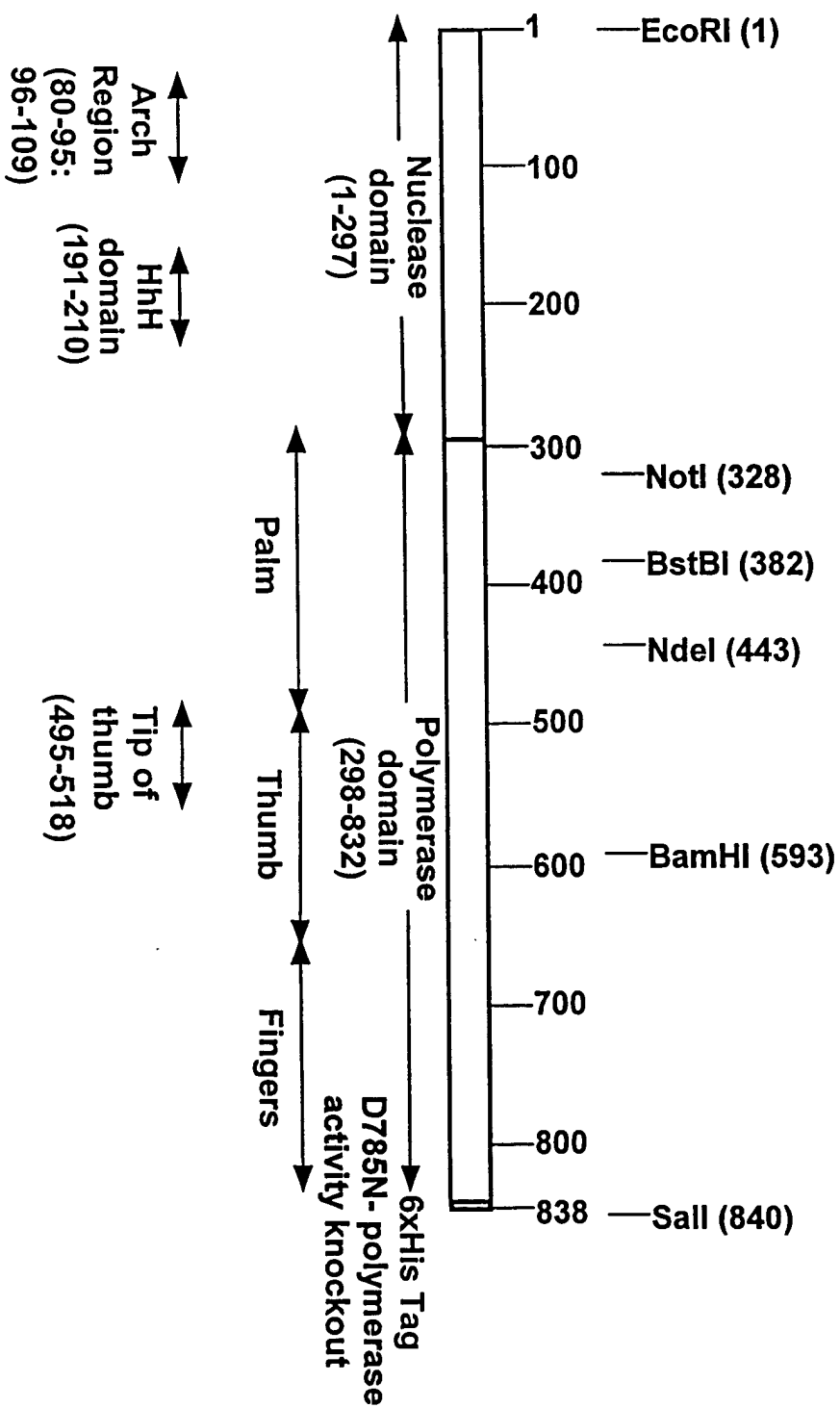


FIGURE 6

004424250

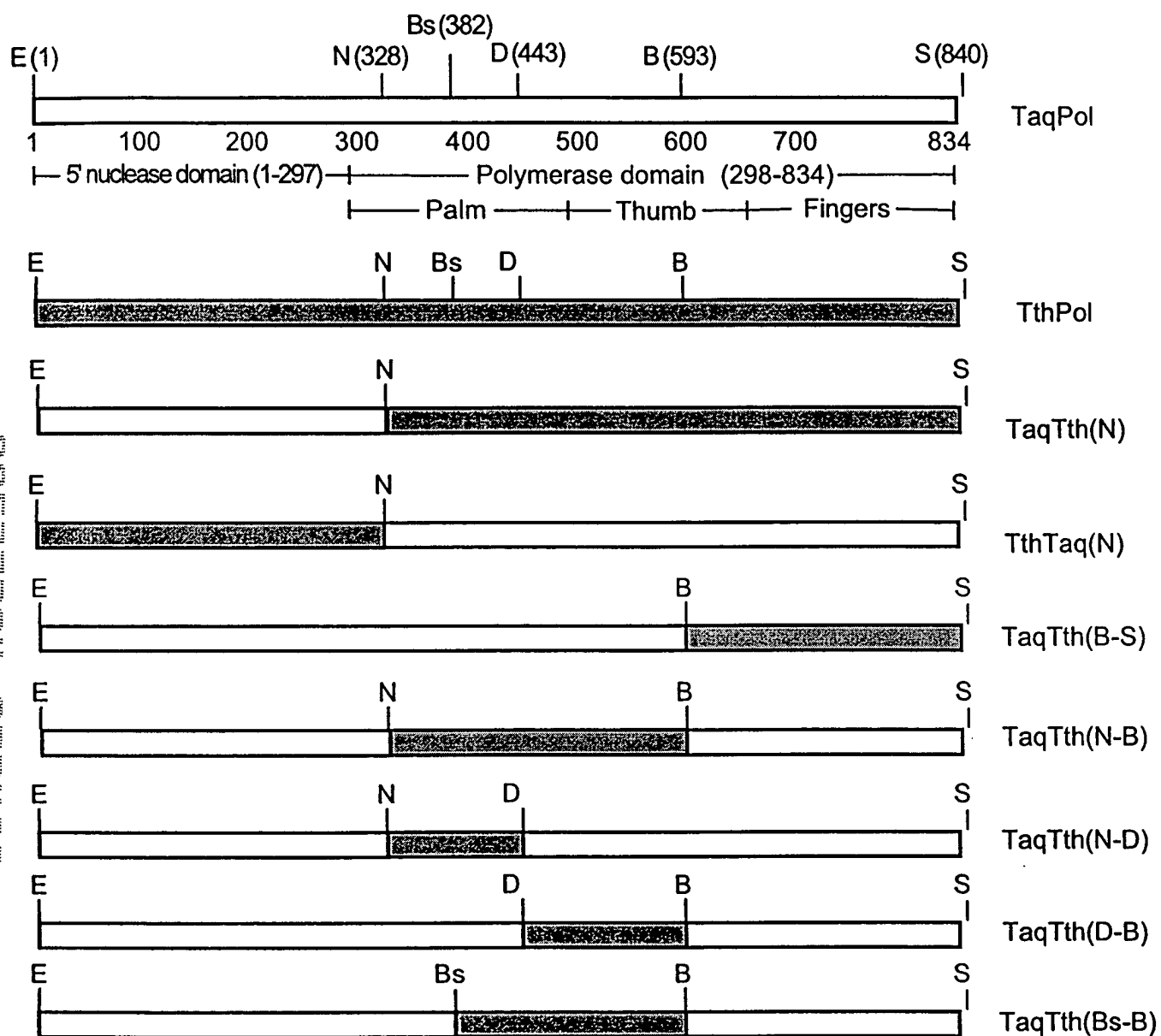


FIGURE 7

FIGURE 8A

MAJORITY [SEQ ID NO:7] ATGXXGGGGATGCTTGGCGTCTTTGAGCGCAAGCGGGTCTCTCTGGTGGAGGGCCACGCTGGCGCT

DNAPTAQ	[SEQ ID NO:1]	. . . AG . G G	G	70
DNAPTFL	[SEQ ID NO:2]	C . G	67
DNAPTHH	[SEQ ID NO:266]	. GA G A	70

MAJORITY ACCGCAGCTTCTTCGGCCCTGAAGGGCCCTCAGCACCGCGGGGGGGAACCGGTGCAGGGCGCTACGGGCTT

DNAPTAQ	CA	G	G	140
DNAPTFL	T	C	C	137
DNAPTTH		G		140

MAJORITY CCGCAAGAGGCTCGTCAAGGGCTGAAGGAGGAGGGGACXXGGGGTGYTGGTCTTGCAGCGGAAG

DNAPTAQC.....A.....	207
DNAPTFLA.....GT..T.....	204
DNAPTTHT..AA..C..CT.....	210

MAJORITY GCGCCGTCCTTCGGCAGGAGGCCTACGAGGCCACAAGCGGGCGGGCCCAAGGGACTTGC

DNAPTAQG. GG.....G.....	277
DNAPTFL	274
DNAPTTHGA.....G.....G.....	280

MAJORITY CCGGGAGGCTCGCCCTCATCAAGGAGCTGGTGGAGCTCCTGGGGCTTGGGGGCTCGAGGTCGGCGGCTA

DNAPTAQA.....G.....G.....	347
DNAPTFLG.....T.....G.....	344
DNAPTHHT.....A.C.....	350

MAJORITY [SEQ ID NO:7] CGAGGGGAGGAGGTGCTGGCCAGCCCTGGCCAAAGAGGGGAAAGGAGGGGTACGAGGTGGGCATCGCTC

DNAPTAQ [SEQ ID NO:1]C.....G.....C.....G..... 417
DNAPTFL [SEQ ID NO:2] T.....G.....CG..... 414
DNAPTTH [SEQ ID NO:266] T..C..... 420

MAJORITY ACGGGGAGCGGAGCGTCTACGAGCTCCTTCGGACCGCATCGCCGTCCTCCACCCGAGGGGTACCTCA

DNAPTAQAAA.....T.....CA..... 487
DNAPTFL ..T.....G.....A.....T.....G. 484
DNAPTTHA..G.C.....G.....CC..... 490

MAJORITY TCACCGGGCGTGGCTTTGGAGAAAGTAGGGCTGAGCGCGGAGGAGTGGGTGGACTACCGGGCGCTGGC

DNAPTAQC.....A.....C.....C.....A. 557
DNAPTFLAC.....C.C..... 554
DNAPTTHA.....C.....T..C.....C.T 560

MAJORITY GGGGAGCGCGTCCGACAACCTCCCGGGGTCAAGGGCATCGGGGAGAAAGCGGGCCXGAAGCTCCTCXAG

DNAPTAQ C.....GAG.....T.....G..GAG.....T..GG.. 627
DNAPTFLG..T..A.....G.....A..G....A..CGG 624
DNAPTTHA.....T.....TC.....A.. 630

MAJORITY GAGTGGGGAGCGCTGGAAAAACCTCCTCAAGAACCTGGACCGGGTGAAGCCCGC---CXTCCGGGAGAGA

DNAPTAQGC.....C.....A..... 694
DNAPTFLT..C..G.....A.....T..T..G.....C 691
DNAPTTHA.....A.....A.AAAA.G..... 700

MAJORITY [SEQ ID NO:7] TCGAGGGCCACATGGAXGAGCTGAXGCTCTCGTGGGAGGCTXTCGAGGCTGGCGACGGAGCCTGCCCGCTGGA

DNAPTAO [SEQ ID NO:1] ...T...C..T...A...C..GG..A... 764
DNAPTFL [SEQ ID NO:2] ...GGG...G.C...GCC..T...C..A...T...A...T... 761
DNAPTTH [SEQ ID NO:266]..A...C...A...C.G...T...C...G...C... 770

MAJORITY GGTGGACTTCGCCAAGXGGGGGAGCCCGACCGGAGGGGCTTAGGGCCCTTCTGGAGAGGCTGGAGCTT

DNAPTAOAA.....A.....T.....T..... 834
DNAPTFLGG.G.C.C..CACA...A...T.....T...GC...T...T...C..T... 831
DNAPTTHC.....C..G.....T.....C.....C.....C..... 840

MAJORITY GGGAGGCTCGTCCAGGAGTTCGGGCTCGTGGAGGGGGCCCAAGGCCCTGGAGGAGGGCCCGCTGCCCGCCCGG

DNAPTAOT....AA..... 904
DNAPTFL ..A.....G..G....GGCA.....T... 901
DNAPTTHC.....C....GGCC..... 910

MAJORITY CGGAAGGGCGCTTCGTGGGCTTGTGCTTTCGGGGCCGAGCGCATGTGGGCGGAGCTTCTGGCGCTGGG

DNAPTAOT.....G.....AAG.....T..... 974
DNAPTFLT..TT.....TC.T.....T..... 971
DNAPTTHC.....C.....G.....AAA..... 980

MAJORITY CCGCGCCAGGGGCGGCTCCACCGGGGACGAGCCCTTTAXGGGCTTAXGGGAGCTXAAGGAGGTG

DNAPTAOG.....C..C..G..T.A..AA..C...G.....G.....C... 1044
DNAPTFL T.GG..GT.....G..CC...T.....A.....G...G.....T...G... 1041
DNAPTTH ...TG.....C.....G.....G.....GGC...G..A..A.....C.....C... 1050

MAJORITY [SEQ ID NO:7] CCGGGXCTGCTGGCCAAAGGACCTGGCCGCTTTGGCCCTGAGGGAGGGGCTXGACCTCTGCGCGGGGACG

DNAPTAQ [SEQ ID NO:1]G..T.....A.....AG.....C.....A.....T..G....GC.....C.... 1114
 DNAPTFL [SEQ ID NO:2]AA.....G.....G.....C.....G.....T..C..A..A.... 1111
 DNAPTTH [SEQ ID NO:266]C.....C.....TC.....G..A.....G.....G..... 1120

MAJORITY ACCCGATGCTCCTCGGCTAGCTGCTGGACCGCTCCAACACACCCCGGAGGGGCTGGCCCGGGCTACGG

DNAPTAQT..... 1184
 DNAPTFLT.....T.....T..... 1181
 DNAPTTHG..... 1190

MAJORITY GCGGGAGTGGACGGAGGAXCGCGGGGAGCGGGGCTCCTXTCCGAGAGGCTCTTCCXGAACCTXXGAG

DNAPTAQG.....G.....T.....GC...T.....GCC....GTG..G. 1254
 DNAPTFLT.....A.....GG....C..G....A..C....AAA.... 1251
 DNAPTTHC..C.CCC.C.....C..G.....CAT..G.....CCTTA.. 1260

MAJORITY CCGCTTGAGGGGAGGAGGGCTCCTTTGGCTTTACGAGGAGGTGGAGAACCCCTTCCGGGGTCCCTGG

DNAPTAQA..G..... 1324
 DNAPTFLA...A..A..AC.C..G.....G.....G.....GCT..... 1321
 DNAPTTHC.....A.....A.....C.....A.....G..... 1330

MAJORITY CCGACATGGAGGGCCAGGGGGTXXCGGGTGGACGTGGGCTAGCTCCAGGGGCTTCCCTGGAGGTGGCGGA

DNAPTAQ 1394
 DNAPTFLGG.....G..C.....T...AG....T..G.....C... 1391
 DNAPTTHC.....C.....A.....T.....T.....C.T..... 1400

FIGURE 8E

MAJORITY [SEQ ID NO:7] GGAGATCGGCGCGCTCGAGGAGGAGGCTCTTCGGCCCTGGCGGGGACGGCCTTCAAGCTCAAGTCCCGGGGAG

DNAPTAO [SEQ ID NO:1]GC.....CC..... 1464
 DNAPTFL [SEQ ID NO:2]G.G....AG..G..... 1461
 DNAPTTH [SEQ ID NO:266]T.....G..... 1470

MAJORITY GAGCTGGAAAGGGTGCTCTTTGACGAGGCTXGGGCTTCGGGCCCATCGGCAAGACGGAGAGACXGGCAAGC

DNAPTAOC.....A..... 1534
 DNAPTFLGC.....G..G..T.....G.....G..G..A.. 1531
 DNAPTTHTA.....T.G..G.....C.A.....A..... 1540

MAJORITY GGTCCAGCAGCGCGCGGTGCTGGAGCGCCCTXCGXGAGCGCCACGCCCATCGTGGAGAAGATCCTGCAGTA

DNAPTAOC.....C..C..... 1604
 DNAPTFLT.....G..A.....CGC..... 1601
 DNAPTTHG.....A..G.....C...C.. 1610

MAJORITY CCGGGAGGCTCAGCAAGCTCAAGAACAGCTAGATXGACCCGCTGCCGXGCCCTCGTCCACCCGAGGACGGGC

DNAPTAOG...G.....T.....G.A...A..... 1674
 DNAPTFLA.....G.C...G.....A...G... 1671
 DNAPTTHG.G.....G..AAG.....G..... 1680

MAJORITY CGCCTCCAGACGGGCTTCAAGCAGACGGGCGCACGGCGAGGCTTAGTAGCTCCGAGCCCAAGCTGC

DNAPTAOA.....A.....T.....C.. 1744
 DNAPTFLG.....C.....TCG..... 1741
 DNAPTTHG.....G..... 1750

MAJORITY [SEQ ID NO:7] AGAAGATCCCGCTCCGGACCCXCTGGGCGAGAGGATCCGCCGGGCCCTTCGTGGCCGAGGAGGGXTGGGT

DNAPTAO [SEQ ID NO:1]G..T..G.....A..C.....G...C. 1814
 DNAPTFL [SEQ ID NO:2]G.....T.....G..C.....A.....C.....C..... 1811
 DNAPTTH [SEQ ID NO:266]CT.....T.....G.....C.....T.....C 1820

MAJORITY GTTGGTGGCCCTGGACTATAGCCAGATAGAGCTCCGGGTGCTGGCCGACCTCTCCGGGGAGGAGAACCTG

DNAPTAO A.....T.....T.....A.....G.....C..... 1884
 DNAPTFLT..T.....G.....T.....T.....C..... 1881
 DNAPTTHT.....T.....G.....C.....A..... 1890

MAJORITY ATCCGGGTCTTCCAGGAGGGAGGACATCCACACCCAGAGCCGACCTGGATGTTCCGGCGTCCGCCCGGG

DNAPTAOT.....C.....GG.....G... 1954
 DNAPTFLT.....T.....TT...C. 1951
 DNAPTTHA.....A.....A..... 1960

MAJORITY AGCGCGTGGAGCCCTGATCCGCCGGGGGGCAAGACCATCAACTTCGGGGTCCCTCTACGGGCATGTCCCG

DNAPTAOA..G..A.....T.....G... 2024
 DNAPTFLA.....T.....G..... 2021
 DNAPTTHA.....GG..G.....G..... 2030

MAJORITY CCACCGCCTCTCCGAGGAGCTTGGCATCCCTACGAGGCGGGTGGCCCTTCATTGAGCGCTACTTCCAG

DNAPTAOA.....T.....CCA.....T... 2094
 DNAPTFLGG.....T.....T..... 2091
 DNAPTTHTA..G.....T.....A.....A 2100

MAJORITY [SEQ ID NO:7] AGCTTCGCCCAAGGTGGGGGCTGGATTGAGAAGACCTGGAGGAGGCGGAGGGGGGTACGTGGAGA

DNAPTAQ [SEQ ID NO:1]

DNAPTFL [SEQ ID NO:2]A.....

DNAPTTH [SEQ ID NO:266].....A.....

2164
2161
2170

MAJORITY CCGTCITCGGGCGGGGGCTACGTGCCCCGACCTCAACGCCCGGGTGAAGAGCGTGGGGGAGGGGGCGGA

DNAPTAQ

DNAPTFL

DNAPTTH

2234
2231
2240

MAJORITY GCGCATGGCCTTCAACATGCCCGTCCAGGGCACGGCGGGGACCTCATGAAGCTGGCCATGGTGAAGCTC

DNAPTAQ

DNAPTFL

DNAPTTH

2304
2301
2310

MAJORITY TTGGCGGGGCTXCAGGAAATGGGGGGCAGGATGCTCCTXCAGGTCCACGAGGAGCTGCTCCTCGAGGGCC

DNAPTAQ

DNAPTFL

DNAPTTH

2374
2371
2380

MAJORITY CCAAAGAGGGGGAGGXGGTGGCGGCTTGGCCCAAGGAGGTCTATGCCCTGGCCGT

DNAPTAQ

DNAPTFL

DNAPTTH

2444
2441
2450

004255 FIGURE 8H 2560

MAJORITY [SEQ ID NO:7] GCGCGCTGGAGGTGGAGGTGGGGATGGGGGAGGAGCTGGCTCTCGCGCCAAGGAGTAG

DNAPTAA	[SEQ ID NO:1]A.....GA	2499
DNAPTFL	[SEQ ID NO:2]CC.....	2496
DNAPTTH	[SEQ ID NO:266]T.....GT...	2505

TAQ PRO	S.	K.	D.	G.	PE. YKA.	A 348
TFL PRO	G. A.	L. SF.		G. WE. L.	Q. R.	G. 347
TTH PRO	A. AP.			K.	C. D.	A. A. K. 350

MAJORITY [SEQ ID NO:8] RGLAKDLAVLALREGLDLXPGDDPML LAYLLDPSNTTPEGVARRYGGEWTE DAGERALLSERLFXNLXX

TAQ PRO	[SEQ ID NO:4]	S	G	P	E	A	A	A	WG	418
TFL PRO	[SEQ ID NO:5]	I	F	E	A	A	QT	KE	417	
TTH PRO	[SEQ ID NO:267]	S	V	AH	HR	LK			420	

MAJORITY RLEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDVAYLQALSLEVAEEIRRELEEVFRLAGHPFNLNSRD

TAQ PRO	R	R	A	R	A	A				488
TFL PRO	K	E	R	EA	V	Q				487
TTH PRO	K	H	L	L						490

MAJORITY OLERVLFDELGLPAIGKTEKTGKRSTSAVLEALREAHPIVEKILQYRELTCLKNTYIDPLPXLVHPRTG

TAQ PRO					S	D	I			558
TFL PRO				DR		A	K			557
TTH PRO	R	L	Q	H	V	S				560

MAJORITY RLHTRFNOTATGRLSSSDPNLQNI PVRTPLGORIRRAFVAEEGWXLVALDYSQIELRVLAHLSGDENL

TAQ PRO				I	L					628
TFL PRO				V	V					627
TTH PRO				A	A					630

MAJORITY IRVFQEGRDIHTQTASWMFGVPPEAVDPLMRRAAKTINFGVLYGMSAHRLSQELAI PYEEAVAFIERYFQ

TAQ PRO	E	R			Q					698
TFL PRO		S	G		G	S				697
TTH PRO	K		V							700

FIGURE 9C

MAJORITY [SEQ ID NO:8] SFPKVRWIEKTL EGRRRGYVETLFGRRRYVPDLNARVKSUREAAERMAFNMPV OGTAADL MKLAMVKL

TAO PRO	[SEQ ID NO:4]E.....	768
TFL PRO	[SEQ ID NO:5]	Y.....G.....R.	767
TTH PRO	[SEQ ID NO:267]K.....	770

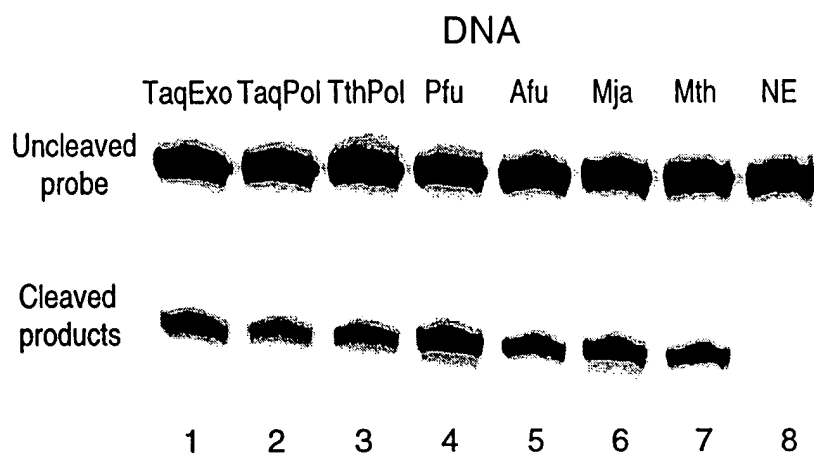
MAJORITY FPRLXEMGARM LQVHDELVL EAPKXRAEXVAA LAKEVMEGVYPLAVPLEVEVGXGEDWLSAKEX

TAO PROE.....E...A...R.....I.....	833
TFL PROO.L.....D...R.....W..O.....L.....	831
TTH PROR.....L....QA...E....A..KA.....M.....G	835

5'-FI-CGAAATTAAATACCTTGTGAGAAGAGTTCA[↓]TdC
 Cleavage site
 Upstream probe
 5'-AGGAGAAGGCACTGGACCGAAGGC
 3'-...GGUCCCUUCCGUUGACCUGGCUUCCGGAACAACCUUCCUCAAGUAUCCAGCCGAG...-5'
 IL-6 RNA target strand
 3'-GGGTCCCTCTTCCGTTGACCCTGGCTTCCGCGAACAACCTCTTCTCAAGTATCG-5'
 IL-6 DNA target strand

FIGURE 10

A



B

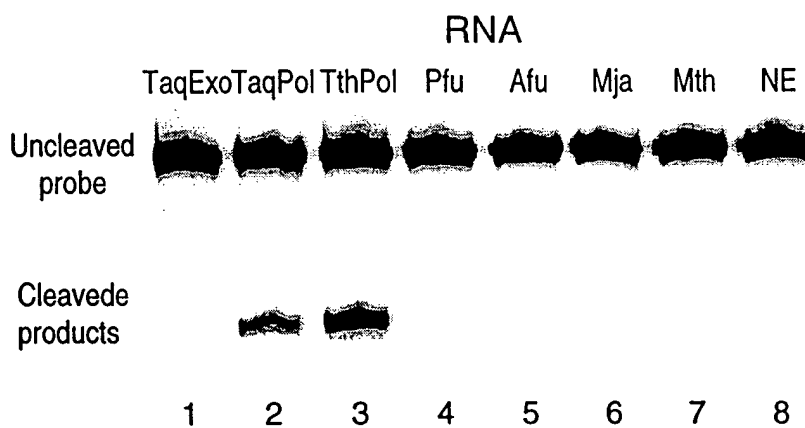


FIGURE 11

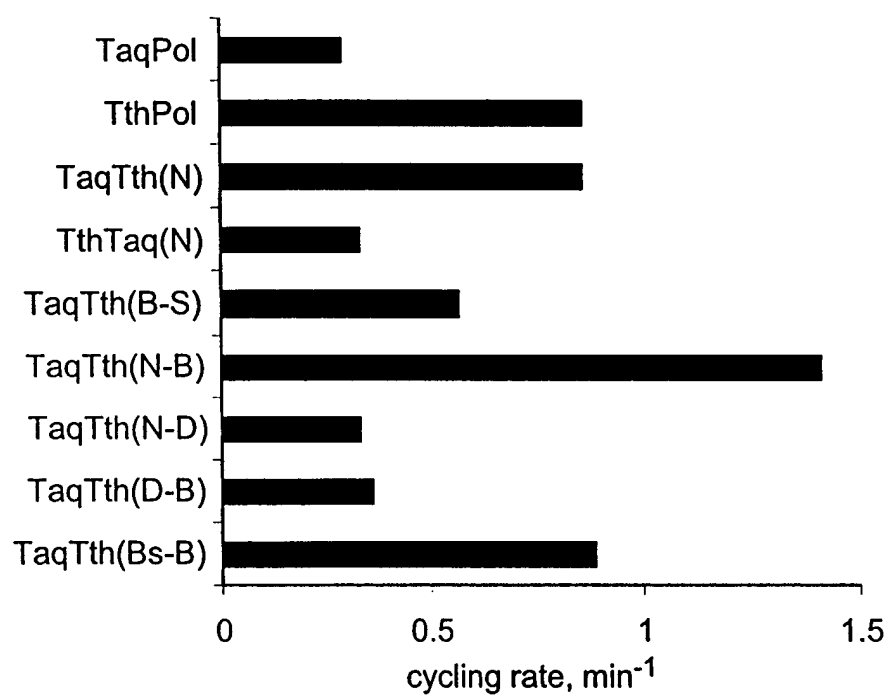


FIGURE 12

	BstBI (382)	390	400	410	420	430	Ndel (443)	440	450	460
1 TaqPol	DPSNTTPEGVARRYGGEWTEEAAGRAALSERL				VNLNWRLEGEERLLWL	YREVERPLS	VLAHMEATGVRLDVA			
2 TthPol	DPSNTTPEGVARRYGGEWTEDAAIRALLSERL				LLENLRLEGEKLLWL	YHEVEKPLS	VLAHMEATGVRLDVA			
				+	++ ++		+		+	+
1 TaqPol	LEVAEEIIRLEAEVFRLAGHPFNLSRDQLERVL	470	480	490	500	510	520	530	540	
2 TthPol	LELAEEIIRLEAEVFRLAGHPFNLSRDQLERVL				FDELGLPALGKT	KTKGRSTSAAVLEALREAHPIVEKILQRELTK				
	+	+	+		+	+			+	
						BamHI (593)				
1 TaqPol	LKSTYIDPLPDLIHPRGTGRHLHTRFNQTATATGR	550	560	570	580	590				
2 TthPol	LKNITYVDPLPDLVHPRTGRHLHTRFNQTATATGR				SSSDPNLNQINIPVRTPLGQRI					
	+	+	+							

FIGURE 13

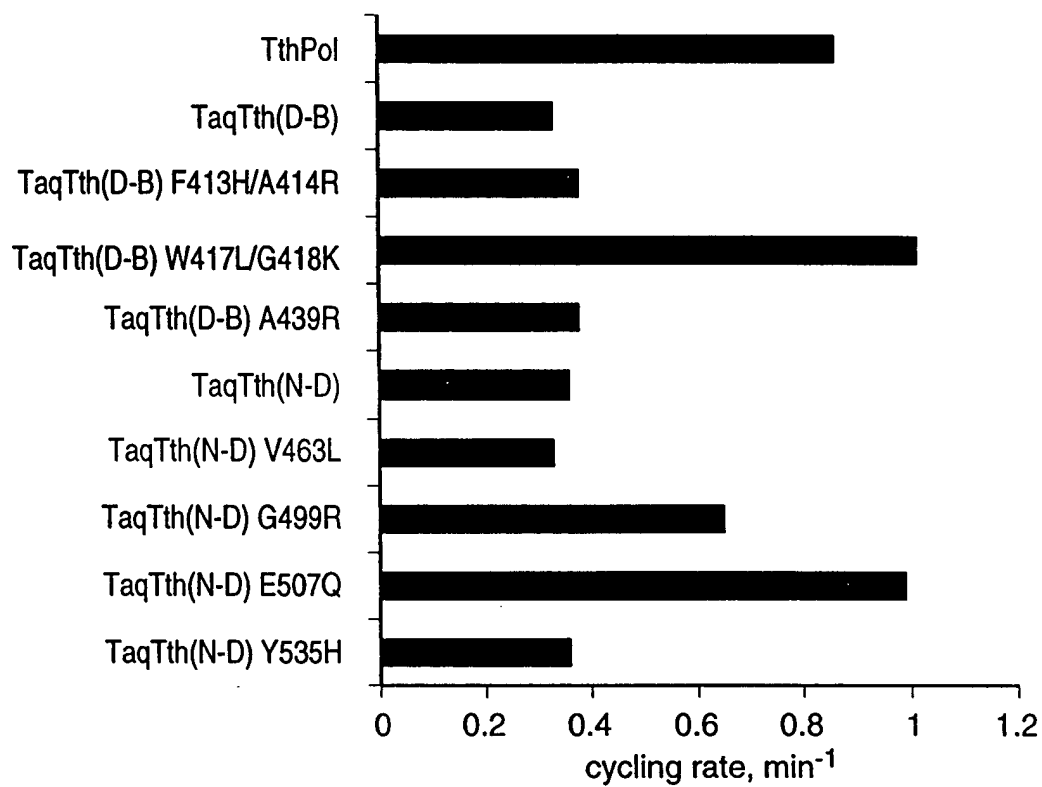


FIGURE 14

0957304.052400

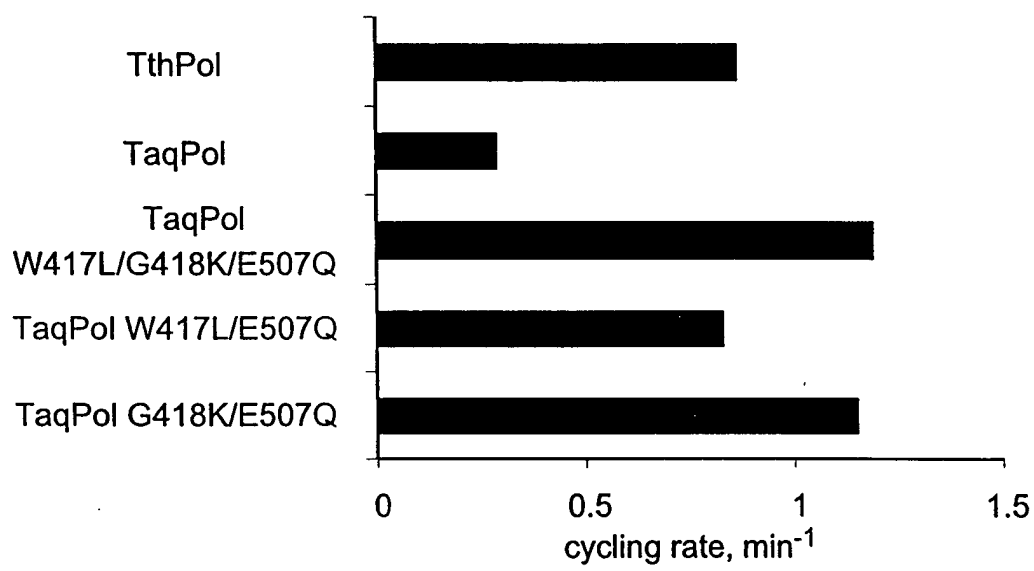


FIGURE 15


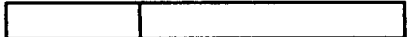



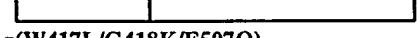
		Polymerase Activity Assays	
		<u>% Fl-labeled dUTP incorporated</u>	
		<u>RNA, p(A) or DNA, p(dA) Template</u>	
Nuclease Domain	Polymerase Domain		
		5.8 (1.00)	14.8 (1.00)
Tth			
		0.8 (0.14)	15.0 (1.01)
Taq			
		4.88 (0.84)	12.9 (0.87)
TaqTth(N)			
		0.58 (0.10)	13.3 (0.90)
TaqTth(N-B)			
		6.60 (1.14)	14.9 (1.01)
TaqTth(B-S)			
		0.42 (0.07)	12.6 (0.85)
Taq(W417L/G418K/E507Q)			

FIGURE 16

004230-402250



FIGURE 17

004250 402450

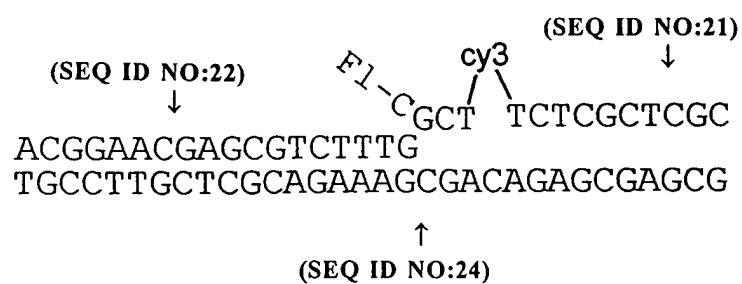


FIGURE 18B

004250" 40642500

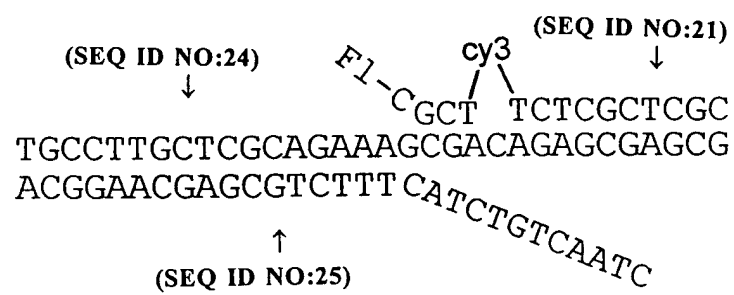


FIGURE 18C

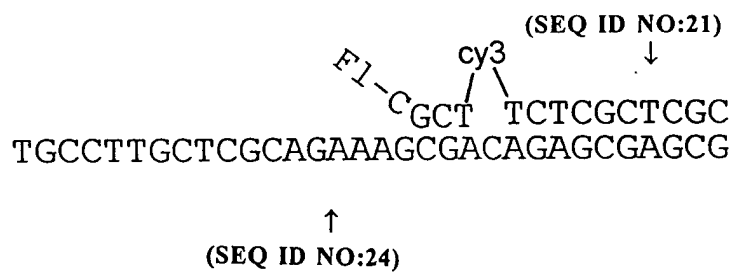


FIGURE 18D

0047309 40042550

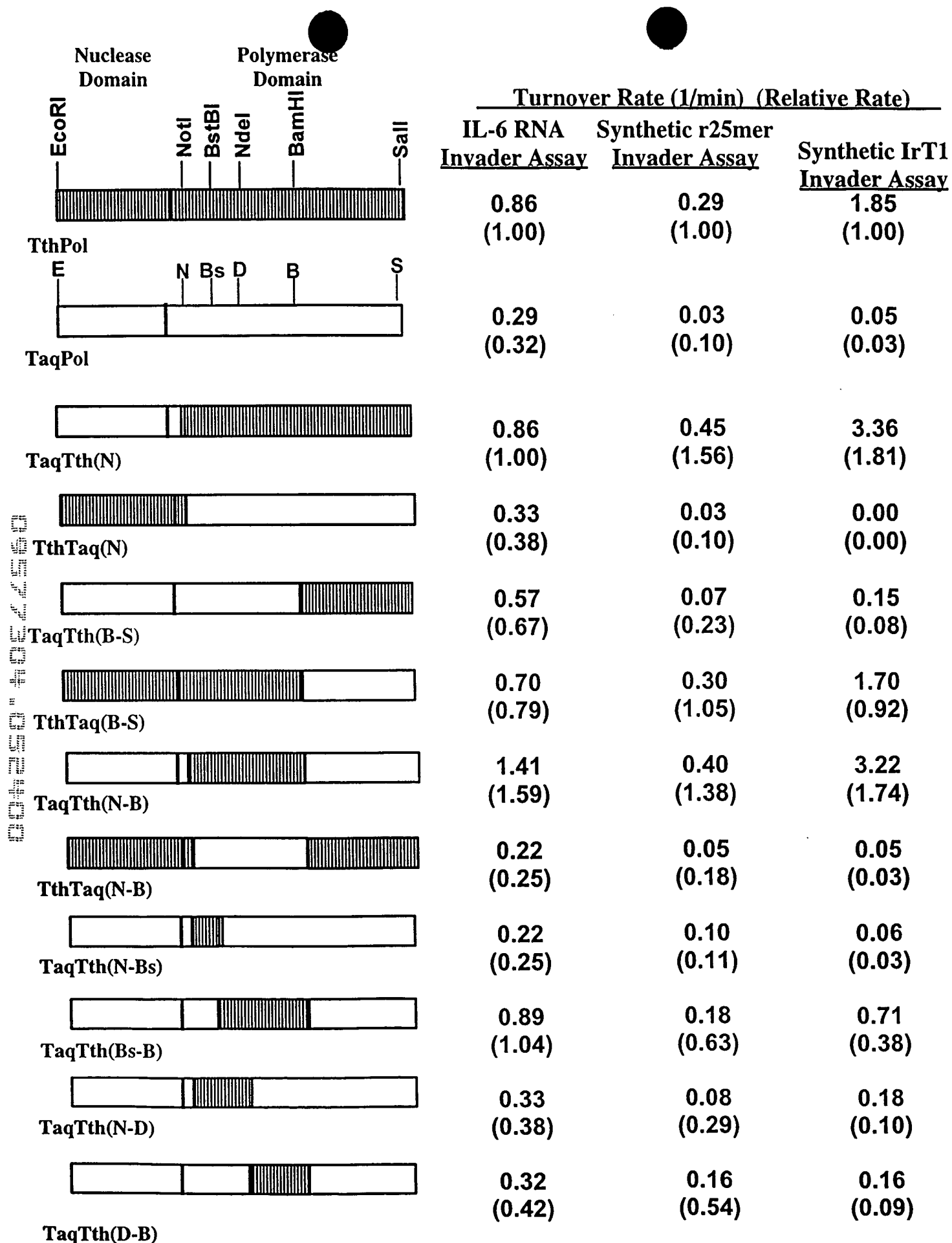


FIGURE 19

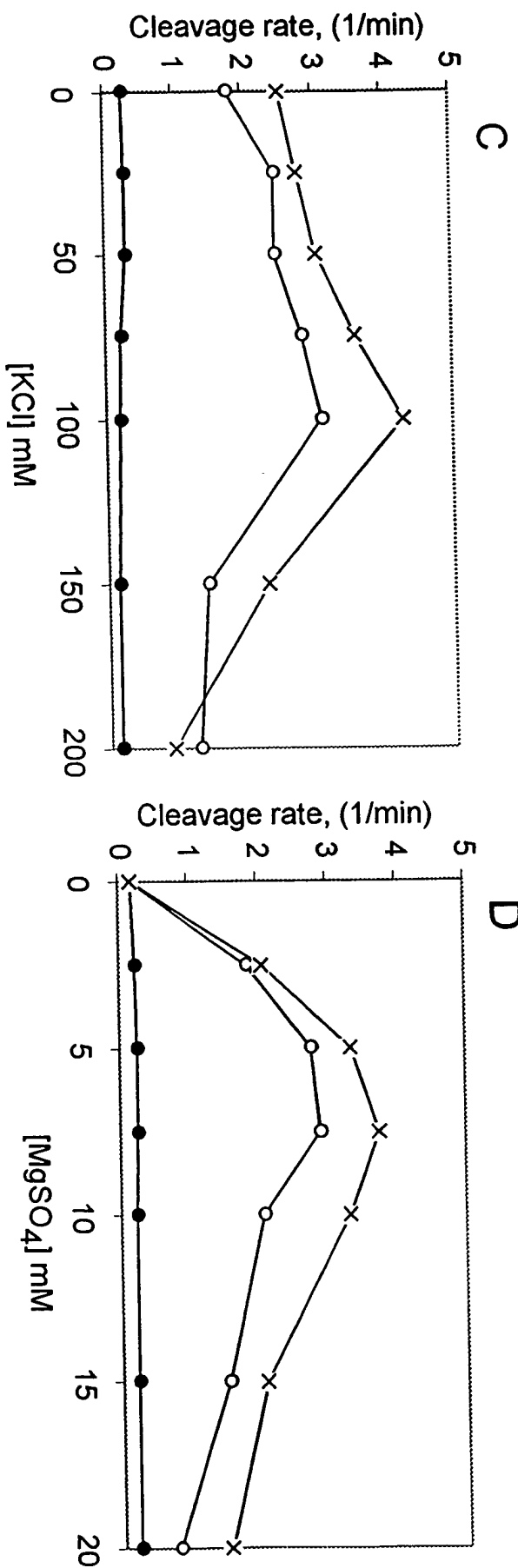
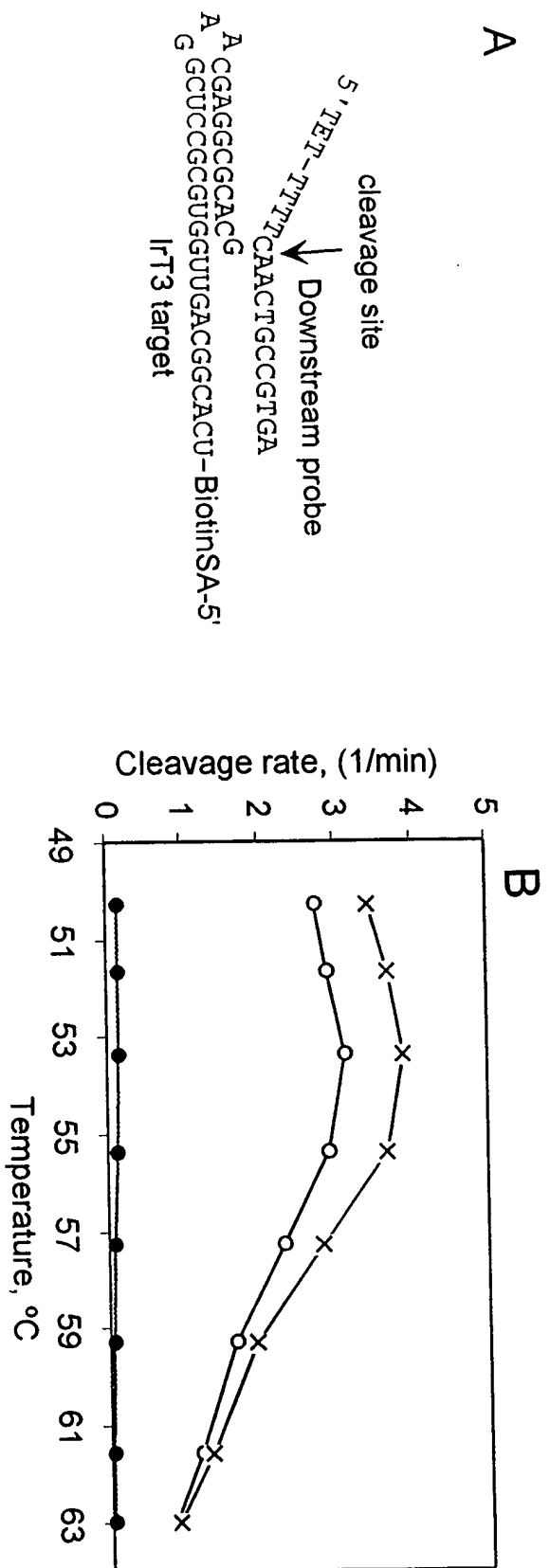


FIGURE 20

09577304.052400

[illegible]

5'-tet-TTTTCAACTGCCGTGA
A CGAGGCGCACG
A GCTCCGCGTGGTTGACGGCACT

5'-tet-TTTTCAACTGCCGTGA
A₁CGAGGCGCACG
A₂GCUCCGCGUGGUUGACGGCACU-BiotinSA-5'

FIGURE 22

A

(SEQ ID NO:29)



3' NH4-AATTGCTCCGCGTGGTTGACGAAGGAGGC-5'

5'-F1-TCCTTCTCAACTGCTTCCTCCG-3'



(SEQ ID NO:30)

B

(SEQ ID NO:31)



5'-AACGAGGCGCACCTCAAATCTCCCTTT-biotin

(SEQ ID NO:29)



3' NH4-AATTGCTCCGCGTGGTTGACGAAGGAGGC-5'

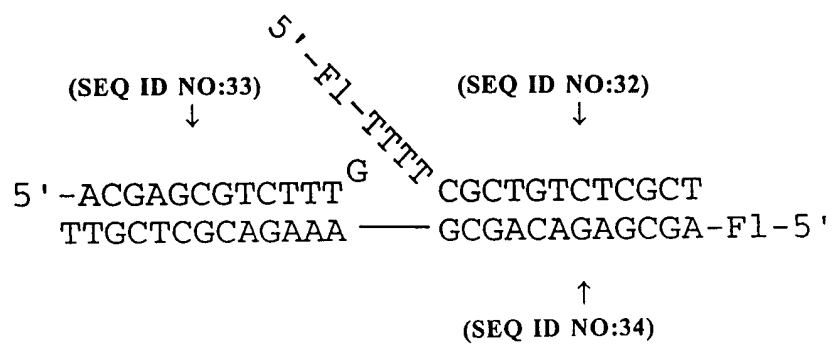
5'-F1-TCCTTCTCAACTGCTTCCTCCG-3'



(SEQ ID NO:30)

004230-4034230

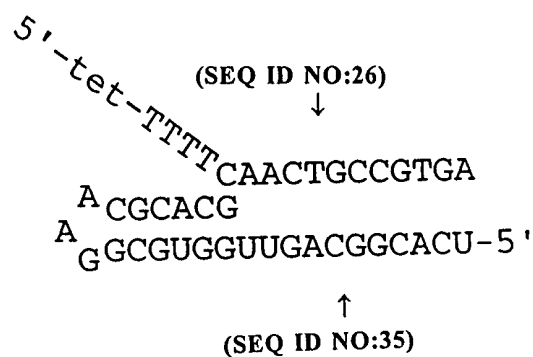
FIGURE 23



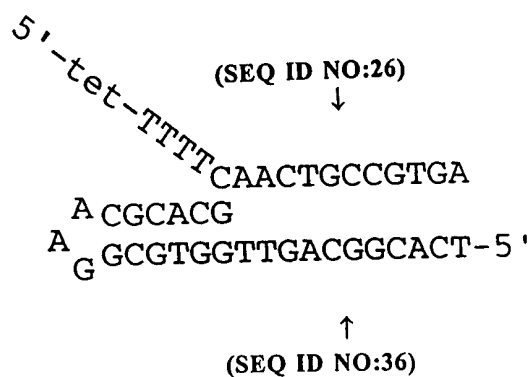
004250"40250

FIGURE 24

A



B



004200 402450

FIGURE 25

